



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANTS: Kerry E. Quinn et al.

SERIAL NUMBER: 09/996,015

EXAMINER: Not yet assigned

FILING DATE: November 28, 2001

ART UNIT: Not yet assigned

FOR: **AORTIC CARBOXYPEPTIDASE-LIKE PROTEINS AND NUCLEIC ACIDS
ENCODING SAME**

Commissioner for Patents
Washington, D.C. 20231

PRELIMINARY AMENDMENT

Prior to examination of the above-identified application, please amend the application as set forth below and consider the following remarks:

In the Specification:

Replace the first full paragraph on page 6:

“FIG. 4 is a comparison showing regions of identity and of conserved amino acid substitutions in the amino acid sequences of a mouse CPPX1 polypeptide (AFO77738) and the ACPL1a polypeptide (SEQ ID NO:2) (ALO35460_GENESCAN_predicted_pep”.”

with the following re-written paragraph:

-- FIG. 4 is a comparison showing regions of identity and of conserved amino acid substitutions in the amino acid sequences of a mouse CPPX1 polypeptide (AFO77738) (SEQ ID NO:13) and the ACPL1a polypeptide (SEQ ID NO:2) (ALO35460_GENESCAN_predicted_pep”).--

A marked-up version showing changes made to the specification is submitted herewith as **Appendix A**, pursuant to 37 C.F.R. § 1.121(b)(1)(iii).

Please insert the sequence listing, pages 1-51, at the end of the specification.

In the Drawings:

Pursuant to 37 C.F.R. § 1.121(d), Applicants submit herewith, in **Appendix B**, separate sheets of drawings showing proposed changes in red. Specifically, Applicants wish to cancel Figure 2 of the present application and insert new Figure 2. Applicants further wish to amend Figures 14, 15, and 16. Applicants respectfully request Examiner's approval of these changes.

Applicants additionally submit herewith, in **Appendix C**, drawings in compliance with 37 C.F.R. § 1.84, incorporating the above changes.

REMARKS

In response to the Notice to File Missing Parts of Nonprovisional Application, Applicants submit herein an initial computer readable form (CRF) copy of the "Sequence Listing," and an initial paper copy of the "Sequence Listing." No new matter has been added. A statement that the content of the paper and computer readable copies are the same and include no new matter, in compliance with 37 C.F.R. §§ 1.821 – 1.825 is also included.

The Specification has been amended to insert the sequence listing and to add a sequence identifier number. Figure 2 of the present application has been canceled because it contains errors. Support for new Figure 2 appears in U.S.S.N. 09/641,741, filed August 18, 2000, (the '741 application). The present application claims priority to the '741 application and incorporates the '741 application by reference (*See, e.g.*, page 1 of the present application). Thus, no new matter has been added.

Additionally, Figures 14-16 misidentify sequences. The drawings have been amended to

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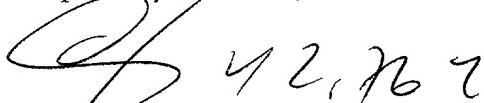
Attorney Docket No.: 15966-581 CIP (Cura-81 CIP)
correct these informalities and to comply with the requirements of 37 C.F.R. § 1.84. No new
matter has been added.

A petition for a two-month extension of time is submitted herewith. Applicants believe
that no additional fee is due with the submission of this Response. However, the Commissioner
is hereby authorized to charge any fees that may be due, or credit any overpayment of same, to
Deposit Account No. 50-0311, Reference No. 15966-581 CIP (Cura-81 CIP).

CONCLUSION

On the basis of the foregoing amendments and remarks, Applicants respectfully submit
that the pending claims are in condition for allowance. If there are any questions regarding this
submission, the Examiner is encouraged to contact the undersigned at the telephone number
provided below.

Respectfully submitted,



Ivor R. Elrifi, Reg. No. 39,529
Attorney for Applicant
c/o MINTZ, LEVIN, COHN, FERRIS,
GLOVSKY & POPEO, P.C.
One Financial Center
Boston, Massachusetts 02111
Tel: (617) 542-6000
Fax: (617) 542-2241

Dated: May 8, 2002

APPENDIX A

In the Specification:

On page 6, first full paragraph:

FIG. 4 is a comparison showing regions of identity and of conserved amino acid substitutions in the amino acid sequences of a mouse CPPX1 polypeptide (AFO77738) (SEQ ID NO:13) and the ACPL1a polypeptide (SEQ ID) (ALO35460_GENESCAN_predicted_pep").

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APPENDIX B
PROPOSED AMENDMENTS TO FIGURES

Cancel

MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETAN
GTSEQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGC
PPLGLESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWC
EEQDA
DPWFQVDAGHPTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSS
GMDAVFPANSDETPVILNLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSD
PNDFLEAPASGSSDPLDFQHHNYKAMRKLMKQVQECPNITRIYSIGKSYQGLKLYVME
MSDKPGEHELGEPEORYEAGMHGNEALGRELLLLLQFLCHEFLRGNPRVTRLSEMRIH
LLPSMNPDGYESIAYHRGSELVGWAEGRWNNQSIDLHNHFADLNTPWEAODDGKVP
HIVPNHHLPLPTYTLPNATVAPETRAVIKWMKRIPFVLSANHGELVVSYPFDMTR
TPWAARELTPTPDDAVFRWLSTVYAGSNLAMQDTSSRRPCHSODFSVHGNIIINGADW
HTVPGSMNDFSYLHTNCFEVTVELSCDKFPHENELPQEENNKDALLYLEQVRMGI
AGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDYWRLLTPGDYMTASAEGYHS
VTRNCRVTFEEGPFCNFVLTKTPKQRLRELLAAGAKVPPDLRRRLERLRGQKD

Fig. 2

Insert

-- **Figure 2. Protein sequence encoded by the coding sequence shown in Figure 1.**

MWGLLLALAFAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETA
NGTSEQHVRIRVIKKKKVIMKKRKKLTLRPTPLVTAGPLVTPTPAGTLDPAEKQET
GCPPLGLESLRVSDSRLEASSQSFGLGPHRGRLNIQSGLEDGDLYDGAWC
EEQDADPWVFQVDAGHPTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGS
RNHSSGMADAVFPANS~~D~~PETPVNL~~L~~PEPQVARFIRLLPQTWLQGGAPCLRAEIL
ACPVSDPN~~D~~LFLEAPASGSSDPLDFQHHNYKAMRKL~~M~~KQVQE~~Q~~CPNITR~~I~~YSIGKSYQ
GLKLYVMEMSDKPGEHELGEPEVRYVAGMHGNEALGRE~~LLL~~MQFLCHEFLRGNPRV
TRL~~L~~SEMRIHLLPSMNPDGYEIA~~Y~~HRGSELVGWAEGRWNNQSIDLNHN~~F~~ADLN~~T~~PLW
EAQDDGKVPHIVPNHHLPLPTYTLPNA~~T~~VAPETRAVIKWMKRIPFVLSANLHGGE
LVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSNLAMQDTSRRPCHSQDF
SVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHENELPQEWENNKD
ALLTYLEQVRMGIAGVVRDKDTELGIADAIAVDGINHDVTTAWGGDYWRLTPG
DYMVTASAEGYHSVTRNCRVTFEEGPFCNFVLTKTPQQLRELLAAGAKVPPDLR
RRLERLRGQKD --

Figure 14.

>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
Length = 734

Score = 2735 (962.8 bits), Expect = 0.0, Sum P(2) = 0.0
Identities = 510/510 (100%), Positives = 510/510 (100%)

Query: 1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQP GTTKVPGSTPALHSSPAQPPAETANGTS 60
MWGLLLALAAFAPAVGPALGAPRNSVLGLAQP GTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct: 1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQP GTTKVPGSTPALHSSPAQPPAETANGTS 60

Query: 61 EQHVRIRVIKKKVIMKKKLTTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 120
EQHVRIRVIKKKVIMKKKLTTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL
Sbjct: 61 EQHVRIRVIKKKVIMKKKLTTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL 120

Query: 121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
Sbjct: 121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Query: 181 PTRFSGVITQGRNSVWRWDWVTSYKVQFSNDSRTWWGSRNHSSGMADVFPANSDPETPVL 240
PTRFSGVITQGRNSVWRWDWVTSYKVQFSNDSRTWWGSRNHSSGMADVFPANSDPETPVL
Sbjct: 181 PTRFSGVITQGRNSVWRWDWVTSYKVQFSNDSRTWWGSRNHSSGMADVFPANSDPETPVL 240

Query: 241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
Sbjct: 241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300

Query: 301 NYKAMRKLMKQVQE QCPNITRIYSIGKS YQGLKLYV MEMSDKPGEHELGEPEVRYVAGMH 360
NYKAMRKLMKQVQE QCPNITRIYSIGKS YQGLKLYV MEMSDKPGEHELGEPEVRYVAGMH
Sbjct: 301 NYKAMRKLMKQVQE QCPNITRIYSIGKS YQGLKLYV MEMSDKPGEHELGEPEVRYVAGMH 360

Query: 361 GNEALGRELLLLMQFLCHEFLRGNPRTVRLSEM RIHLLPSMNP DGYEIAYHRGSELVG 420
GNEALGRELLLLMQFLCHEFLRGNPRTVRLSEM RIHLLPSMNP DGYEIAYHRGSELVG
Sbjct: 361 GNEALGRELLLLMQFLCHEFLRGNPRTVRLSEM RIHLLPSMNP DGYEIAYHRGSELVG 420

Query: 421 WAEGRWNNQSIDLHNHFADLNTP LWEAQDDGKVP HIVPNHHLPLPTYYTLPNATVAPETR 480
WAEGRWNNQSIDLHNHFADLNTP LWEAQDDGKVP HIVPNHHLPLPTYYTLPNATVAPETR
Sbjct: 421 WAEGRWNNQSIDLHNHFADLNTP LWEAQDDGKVP HIVPNHHLPLPTYYTLPNATVAPETR 480

Query: 481 AVIKWMKRIPFVLSANLHGGLVVSY PFDM 510 (SEQ ID NO: 45)
AVIKWMKRIPFVLSANLHGGLVVSY PFDM
Sbjct: 481 AVIKWMKRIPFVLSANLHGGLVVSY PFDM 510

Score = 341 (120.0 bits), Expect = 0.0, Sum P(2) = 0.0
Identities = 67/69 (97%), Positives = 67/69 (97%)

Query: 507 PFD-MVTASAEGYHSVTRNCRVTFEEGPFP CNFVLTKTPKQRLRELLAAGAKVPPDLRRR 565
P D MVTASAEGYHSVTRNCRVTFEEGPFP CNFVLTKTPKQRLRELLAAGAKVPPDLRRR
Sbjct: 666 PGDYMVTASAEGYHSVTRNCRVTFEEGPFP CNFVLTKTPKQRLRELLAAGAKVPPDLRRR 725

Query: 566 LERLRGQKD 574 (SEQ ID NO: 6) (SEQ ID NO: 46)
LERLRGQKD (SEQ ID NO: 41)
Sbjct: 726 LERLRGQKD 734 (SEQ ID NO: 42)

Figure 15

>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
Length = 734

Score = 1005 (353.8 bits), Expect = 4.4e-101, P = 4.4e-101
Identities = 192/193 (99%), Positives = 193/193 (100%)

Query: 1 MWGLLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
MWGLLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct: 1 MWGLLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query: 61 EQHVRIRVIKKKVIMKKRKLLTRPTPLVTAGPLVTPTPAGTLDPDAEKQETGCPPGL 120
EQHVRIRVIKKKVIMKKRKLLTRPTPLVTAGPLVTPTPAGTLDPDAEKQETGCPPGL
Sbjct: 61 EQHVRIRVIKKKVIMKKRKLLTRPTPLVTAGPLVTPTPAGTLDPDAEKQETGCPPGL 120

Query: 121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCCEEQDADPWFQVDAGH 180
ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCCEEQDADPWFQVDAGH
Sbjct: 121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCCEEQDADPWFQVDAGH 180

Query: 181 PTRFSGVITQGRD 193 [(SEQ ID NO:8)] (SEQ ID NO:47)
PTRFSGVITQGR+ (SEQ ID NO:43)
Sbjct: 181 PTRFSGVITQGRN 193 (SEQ ID NO:44)

Figure 16

>ptnr:SPTRREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
Length = 734

Score = 3952 (1391.2 bits), Expect = 0.0, P = 0.0
Identities = 734/734 (100%), Positives = 734/734 (100%)

Query: 1 MWGLLLALAAFAFAPAVGPALGAPRNSVLGLAQPGTTKVGSTPAHLHSSPAQPPAETANGTS 60
MWGLLLALAAFAFAPAVGPALGAPRNSVLGLAQPGTTKVGSTPAHLHSSPAQPPAETANGTS
Sbjct: 1 MWGLLLALAAFAFAPAVGPALGAPRNSVLGLAQPGTTKVGSTPAHLHSSPAQPPAETANGTS 60

Query: 61 EQHVRIRVIKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDAEKQETGCPLLGL 120
EQHVRIRVIKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDAEKQETGCPLLGL
Sbjct: 61 EQHVRIRVIKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDAEKQETGCPLLGL 120

Query: 121 ESLRVSDSRLEASSQSFGGLGPHGRRLNIQSGLEDGDLYDGAWC AEEQDADPWFQVDAGH 180
ESLRVSDSRLEASSQSFGGLGPHGRRLNIQSGLEDGDLYDGAWC AEEQDADPWFQVDAGH
Sbjct: 121 ESLRVSDSRLEASSQSFGGLGPHGRRLNIQSGLEDGDLYDGAWC AEEQDADPWFQVDAGH 180

Query: 181 PTRFSGVITQGRNSVWRWDWVTSYKVQFSNDSRTTWGSRNHSSGMDAVFPANSDPETPVL 240
PTRFSGVITQGRNSVWRWDWVTSYKVQFSNDSRTTWGSRNHSSGMDAVFPANSDPETPVL
Sbjct: 181 PTRFSGVITQGRNSVWRWDWVTSYKVQFSNDSRTTWGSRNHSSGMDAVFPANSDPETPVL 240

Query: 241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
Sbjct: 241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300

Query: 301 NYKAMRKLMKQVQEQQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360
NYKAMRKLMKQVQEQQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH
Sbjct: 301 NYKAMRKLMKQVQEQQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360

Query: 361 GNEALGRELLLLMQFLCHEFLRGNPVRTLLSEMRIIHLPSMNPDGYEIA YHRGSELVG 420
GNEALGRELLLLMQFLCHEFLRGNPVRTLLSEMRIIHLPSMNPDGYEIA YHRGSELVG
Sbjct: 361 GNEALGRELLLLMQFLCHEFLRGNPVRTLLSEMRIIHLPSMNPDGYEIA YHRGSELVG 420

Query: 421 WAEGRWNNSQISIDLHNHFADLNTPLWEAQDDGKVPHVNVHHLPLPTYYTLPNATVAPETR 480
WAEGRWNNSQISIDLHNHFADLNTPLWEAQDDGKVPHVNVHHLPLPTYYTLPNATVAPETR
Sbjct: 421 WAEGRWNNSQISIDLHNHFADLNTPLWEAQDDGKVPHVNVHHLPLPTYYTLPNATVAPETR 480

Query: 481 AVIKWMKRIPFVLSANLHGGELVVSVYFPDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540
AVIKWMKRIPFVLSANLHGGELVVSVYFPDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
Sbjct: 481 AVIKWMKRIPFVLSANLHGGELVVSVYFPDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540

Query: 541 LAMQDTSSRRPCHSQDFSVHGNINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600
LAMQDTSSRRPCHSQDFSVHGNINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
Sbjct: 541 LAMQDTSSRRPCHSQDFSVHGNINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600

Query: 601 NELPQEENNKKDALLTLEQVRMGIAGVVRDKTELGIADAVIADVGINHDVTTAWGGDY 660
NELPQEENNKKDALLTLEQVRMGIAGVVRDKTELGIADAVIADVGINHDVTTAWGGDY
Sbjct: 601 NELPQEENNKKDALLTLEQVRMGIAGVVRDKTELGIADAVIADVGINHDVTTAWGGDY 660

Query: 661 WRLLTPGDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720
WRLLTPGDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
Sbjct: 661 WRLLTPGDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720

Query: 721 DLRRRLERLRGQKD 734 (SEQ ID NO:2)
DLRRRLERLRGQKD [(SEQ ID NO:45)]
Sbjct: 721 DLRRRLERLRGQKD 734 [(SEQ ID NO:46)]

APPENDIX C
SUBSTITUTE DRAWINGS